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(b) identifying a second bi-ligand to a second enzyme in said enzyme family, wherein said bi-ligand comprises said common ligand and a third ligand, wherein said third ligand binds to a substrate binding site of said second enzyme; and

(c) generating a bi-target ligand comprising said common ligand, said second ligand and said third ligand, whereby said bi-target ligand can bind to said first enzyme and said second enzyme.

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43. (New) The method of claim 42, wherein said enzyme is selected from the group consisting of kinases, dehydrogenases, oxidoreductases, GTPases, carboxyl transferases, acyl transferases, decarboxylases, transaminases, racemases, methyl transferases, formyl transferases, and α -ketodecarboxylases.

44. (New) The method of claim 42, wherein said enzyme family binds a cofactor selected from the group consisting of nicotinamide adenine dinucleotide, nicotinamide adenine dinucleotide phosphate, thiamine pyrophosphate, flavin adenine dinucleotide, flavin mononucleotide, pyridoxal phosphate, coenzyme A, tetrahydrofolate, adenosine triphosphate, guanosine triphosphate and S-adenosyl methionine.

45. (New) The method of claim 42, wherein said second ligand and said third ligand are attached to said common ligand by a linker having approximate C2 symmetry.

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46. (New) The method of claim 45, wherein said second ligand and said third ligand are attached to said common ligand by a linker having perfect C2 symmetry.

47. (New) A method for identifying a bi-target ligand to enzymes in an enzyme family, comprising:

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(a) identifying a first bi-ligand to a first enzyme in said enzyme family, wherein said bi-ligand comprises a common ligand, wherein said common ligand is a cofactor or mimic thereof, and a second ligand, wherein said second ligand binds to a substrate binding site of said first enzyme, wherein said enzyme family comprises two or more enzymes that bind to the same cofactor;

(b) identifying a second bi-ligand to a second enzyme in said enzyme family, wherein said bi-ligand comprises said common ligand and a third ligand, wherein said third ligand binds to a substrate binding site of said second enzyme; and

(c) generating a bi-target ligand comprising said common ligand, said second ligand and said third ligand, whereby said bi-target ligand can bind to said first enzyme and said second enzyme.

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48. (New) The method of claim 47, wherein said enzyme is selected from the group consisting of kinases, dehydrogenases, oxidoreductases, GTPases, carboxyl transferases, acyl transferases, decarboxylases, transaminases, racemases, methyl transferases, formyl transferases, and α -ketodecarboxylases.

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COT 49. (New) The method of claim 47, wherein said enzyme family binds a cofactor selected from the group consisting of nicotinamide adenine dinucleotide, nicotinamide adenine dinucleotide phosphate, thiamine pyrophosphate, flavin adenine dinucleotide, flavin mononucleotide, pyridoxal phosphate, coenzyme A, tetrahydrofolate, adenosine triphosphate, guanosine triphosphate and S-adenosyl methionine.

50. (New) The method of claim 47, wherein said second ligand and said third ligand are attached to said common ligand by a linker having approximate C2 symmetry.

51. (New) The method of claim 50, wherein said second ligand and said third ligand are attached to said common ligand by a linker having perfect C2 symmetry.

52. (New) A method for identifying a bi-target ligand to enzymes in an enzyme family, comprising:

(a) identifying a first bi-ligand to a first enzyme in said enzyme family, wherein said bi-ligand comprises a common ligand, wherein said common ligand binds to a cofactor binding

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site, and a second ligand, wherein said second ligand binds to a substrate binding site of said first enzyme;

(b) identifying a second bi-ligand to a second enzyme in said enzyme family, wherein said bi-ligand comprises said common ligand and a third ligand, wherein said third ligand binds to a substrate binding site of said second enzyme; and

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(c) generating a bi-target ligand comprising said common ligand, said second ligand and said third ligand, whereby said bi-target ligand can bind to said first enzyme and said second enzyme.

53. (New) The method of claim 52, wherein said enzyme is selected from the group consisting of kinases, dehydrogenases, oxidoreductases, GTPases, carboxyl transferases, acyl transferases, decarboxylases, transaminases, racemases, methyl transferases, formyl transferases, and α -ketodecarboxylases.

54. (New) The method of claim 52, wherein said enzyme family binds a cofactor selected from the group consisting of nicotinamide adenine dinucleotide, nicotinamide adenine dinucleotide phosphate, thiamine pyrophosphate, flavin adenine dinucleotide, flavin mononucleotide, pyridoxal phosphate, coenzyme A, tetrahydrofolate, adenosine triphosphate, guanosine triphosphate and S-adenosyl methionine.

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55. (New) The method of claim 52, wherein said second ligand and said third ligand are attached to said common ligand by a linker having approximate C2 symmetry.

56. (New) The method of claim 55, wherein said second ligand and said third ligand are attached to said common ligand by a linker having perfect C2 symmetry.

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57. (New) A method for identifying a bi-target ligand to enzymes in an enzyme family, comprising:

(a) identifying a first bi-ligand to a first enzyme in said enzyme family, wherein said bi-ligand comprises a common ligand, wherein said common ligand binds to a cofactor binding site and competes for cofactor binding, and a second ligand, wherein said second ligand binds to a substrate binding site of said first enzyme;

(b) identifying a second bi-ligand to a second enzyme in said enzyme family, wherein said bi-ligand comprises said common ligand and a third ligand, wherein said third ligand binds to a substrate binding site of said second enzyme; and

(c) generating a bi-target ligand comprising said common ligand, said second ligand and said third ligand, whereby said bi-target ligand can bind to said first enzyme and said second enzyme.

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58. (New) The method of claim 57, wherein said is enzyme selected from the group consisting of kinases, dehydrogenases, oxidoreductases, GTPases, carboxyl transferases, acyl transferases, decarboxylases, transaminases, racemases, methyl transferases, formyl transferases, and α -ketodecarboxylases.

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59. (New) The method of claim 57, wherein said enzyme family binds a cofactor selected from the group consisting of nicotinamide adenine dinucleotide, nicotinamide adenine dinucleotide phosphate, thiamine pyrophosphate, flavin adenine dinucleotide, flavin mononucleotide, pyridoxal phosphate, coenzyme A, tetrahydrofolate, adenosine triphosphate, guanosine triphosphate and S-adenosyl methionine.

60. (New) The method of claim 57, wherein said second ligand and said third ligand are attached to said common ligand by a linker having approximate C2 symmetry.

61. (New) The method of claim 60, wherein said second ligand and said third ligand are attached to said common ligand by a linker having perfect C2 symmetry.

REMARKS

Claims 15-19 and 37-41 are pending. New claims 42-61 have been added. Support for the new claims can be found throughout the specification and in the claims as filed. In particular, support for the new claims can be found, for example,